AMENDMENTS

Amendments to the claims:

This listing of claims will replace all prior versions, and listings, of claims in the application.

Claims 1-27 (cancelled)

28. (New) A computer program product for generating a protein sequence, the computer program product including a computer readable medium encoded with a program module, the program module including instructions directing at least one processor to:

a) receive coordinates for a three dimensional protein backbone structure with variable residue positions;

b) establish a group of potential rotamers for each of said variable residue positions, wherein at least one variable residue position has rotamers from at least two different amino acid side chains; and

c) analyze the interaction of each of said rotamers with all or part of the remainder of said protein backbone structure to generate a set of optimized protein sequences, the instructions to analyze including instructions to perform a HERO search comprising:

i) a Goldstein singles dead end elimination (DEE) applied iteratively until no further rotamers can be eliminated;

ii) a split singles DEE (s = 1) applied iteratively until no further rotamers can be eliminated;

iii) a singles bounding criterion once for each rotamer; and

iv) apply one of the following during each cycle:

magic bullet Goldstein doubles once for each rotamer pair,

Monte Carlo search to find $E_{reference}$ from a valid conformation followed by doubles bounding criterion once for each rotamer pair,

full Goldstein doubles once for each rotamer pair using q_{rs} and q_{uv} metrics, and,

unification of residues with the highest fraction of dead-ending pairs.

29. (New) A computer program according to claim 28 wherein the split singles DEE comprises a magic bullet metric.

30. (New) A computer program according to claim 28 wherein said set of optimized protein sequences comprises the globally optimal protein sequence.

31. (New) A computer program according to claim 28 wherein said analyzing step includes instruction to use of at least one scoring function, wherein said scoring function is selected from the group consisting of van der Waals potential scoring function, a hydrogen bond potential scoring function, an atomic solvation scoring function, an electrostatic scoring function, and a secondary structure propensity scoring function.

32. (New) A computer program according to claim 33 wherein said atomic solvation scoring function includes a scaling factor that compensates for over-counting.

33. (New) A computer program according to claim 30 further comprising generating a list of additional optimal sequences from said globally optimal protein sequence.

34. (New) A computer program according to claim 33 wherein said generating includes the use of a Monte Carlo search.

35. (New) A microprocessor coupled to a computer readable medium encoded with a program module, the microprocessor configured to:

a) receive coordinates for a three dimensional protein backbone structure with variable residue positions;

b) establish a group of potential rotamers for each of said variable residue positions, wherein at least one variable residue position has rotamers from at least two different amino acid side chains; and

c) analyze the interaction of each of said rotamers with all or part of the remainder of said protein backbone structure to generate a set of optimized protein sequences, the instructions to analyze including instructions to perform a HERO search comprising:

i) a Goldstein singles dead end elimination (DEE) applied iteratively until no further rotamers can be eliminated;

ii) a split singles DEE (s = 1) applied iteratively until no further rotamers can be eliminated;

iii) a singles bounding criterion once for each rotamer; and

iv) apply one of the following during each cycle:

magic bullet Goldstein doubles once for each rotamer pair,

Monte Carlo search to find $E_{reference}$ from a valid conformation followed by doubles bounding criterion once for each rotamer pair,

full Goldstein doubles once for each rotamer pair using q_{rs} and q_{uv} metrics, and,

unification of residues with the highest fraction of dead-ending pairs.

36. (New) A microprocessor according to claim 35 wherein the split singles DEE comprises a magic bullet metric.

37. (New) A microprocessor according to claim 35 wherein said set of optimized protein sequences comprises the globally optimal protein sequence.

38. (New) A microprocessor according to claim 35 wherein said analyzing step includes instruction to use of at least one scoring function, wherein said scoring function is selected from the group consisting of van der Waals potential scoring function, a hydrogen bond potential scoring function, an atomic solvation scoring function, an electrostatic scoring function, and a secondary structure propensity scoring function.

39. (New) A microprocessor according to claim 38 wherein said atomic solvation scoring function includes a scaling factor that compensates for over-counting.

40. (New) A microprocessor according to claim 37 further comprising generating a list of additional optimal sequences from said globally optimal protein sequence.

41. (New) A microprocessor according to claim 40 wherein said generating includes the use of a Monte Carlo search.

42. (New) A method for determining a protein sequence, the method comprising:

transmitting coordinates for a three-dimensional protein backbone structure with variable residue positions to a microprocessor configured to establish a group of potential rotamers for each of said variable residue positions, wherein at least one variable residue position has rotamers from at least two different amino acid side chains, the microprocessor further configured to analyze the interaction of each of said rotamers with all or part of the remainder of said protein backbone structure, including providing instructions to perform a HERO search to generate a set of optimized protein sequences, said instructions comprising:

i) a Goldstein singles dead end elimination (DEE) applied iteratively until no further rotamers can be eliminated;

ii) a split singles DEE (s = 1) applied iteratively until no further rotamers can be eliminated;

iii) a singles bounding criterion once for each rotamer; and

iv) apply one of the following during each cycle:

magic bullet Goldstein doubles once for each rotamer pair,

Monte Carlo search to find $E_{reference}$ from a valid conformation followed by doubles bounding criterion once for each rotamer pair,

full Goldstein doubles once for each rotamer pair using q_{rs} and q_{uv} metrics, and,

unification of residues with the highest fraction of dead-ending pairs.

43. (New) A method according to claim 42 wherein the set of optimized protein sequences is displayed on a display device.

44. (New) A method according to claim 42 wherein the set of optimized protein sequences stored on a computer readable storage medium.

45. (New) A computer readable memory encoded with a program module to direct a computer to function in a specified manner, the program module comprising:

a) a side chain module comprising instructions directing the computer to correlate a group of potential rotamers for residue positions of a protein backbone model;

b) a ranking module comprising instructions directing the computer to analyze the interaction of each of said rotamers with all or part of the remainder of said protein to generate a set of optimized protein sequences wherein said instructions to analyze include instructions to perform a HERO search comprising:

i) a Goldstein singles dead end elimination (DEE) applied iteratively until no further rotamers can be eliminated;

ii) a split singles DEE (s = 1) applied iteratively until no further rotamers can be eliminated;

iii) a singles bounding criterion once for each rotamer; and

iv) apply one of the following during each cycle:

magic bullet Goldstein doubles once for each rotamer pair,

Monte Carlo search to find $E_{reference}$ from a valid conformation followed by doubles bounding criterion once for each rotamer pair,

full Goldstein doubles once for each rotamer pair using q_{rs} and q_{uv} metrics, and,

unification of residues with the highest fraction of dead-ending pairs.

46. (New) A computer readable memory according to claim 45 wherein said analyzing step includes instruction to use of at least one scoring function wherein said scoring function is selected from the group consisting of a Van der Waals potential scoring function, a hydrogen bond potential scoring function, an atomic solvation scoring function, an electrostatic scoring function and a secondary structure propensity scoring function.

47. (New) A computer readable memory according to claim 45 further comprising an assessment module to assess the correspondence between potential energy test results and theoretical potential energy data.